



#4

SEQUENCE LISTING

<110> Arnaut, Greta
Boets, Annette
Vanneste, Stefaan
Van Rie, Jeroen
Van Houdt, Sara

<120> Novel *Bacillus thuringiensis* insecticidal proteins

<130> 58764.000036

<140> US 10/040,906

<141> 2002-01-09

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<170> PatentIn version 3.1

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96

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Thr Ile Arg Lys Glu Trp Met Glu Trp Lys Arg Thr Asp His Ser Leu
35 40 45

144

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Tyr Val Ala Pro Ile Val Gly Thr Val Ser Ser Phe Leu Leu Lys Lys
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192

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65 70 75 80

240

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Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala Arg
100 105 110

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Val Asn Ala Glu Leu Glu Gly Leu Gln Ala Asn Ile Arg Glu Phe Asn

384

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ctc aat gca gat gaa tgg gga att tca gca gca aca tta cgt acg tat Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr Tyr 195	200	205	624
caa aat tat ctg aaa aat tat aca aca gag tac tct aat tat tgt ata Gln Asn Tyr Leu Lys Asn Tyr Thr Glu Tyr Ser Asn Tyr Cys Ile 210	215	220	672
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gct aat tta tat gca agc ggt agt gga cca cag cag act caa tca ttt Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser Phe 275	280	285	864
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Thr Phe Asn Ser Gly Thr Gln Phe Glu Leu Met Asn Ile Met Phe Val																																																																																																																									
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620																																																																																																																									
cca act aat ctt cca cca ata tat taa	1899																																																																																																																								
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Asn Val Val Ala His Asp Pro Phe Ser Phe Glu His Lys Ser Leu Asp																																																																																																																									
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Thr Ile Arg Lys Glu Trp Met Glu Trp Lys Arg Thr Asp His Ser Leu																																																																																																																									
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Tyr Val Ala Pro Ile Val Gly Thr Val Ser Ser Phe Leu Leu Lys Lys																																																																																																																									
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Val Gly Ser Leu Ile Gly Lys Arg Ile Leu Ser Glu Leu Trp Gly Leu																																																																																																																									
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Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg Glu																																																																																																																									
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Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala Arg																																																																																																																									
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Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn Arg																																																																																																																									
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180

185

190

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Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu Val Val
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Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile Arg Asn
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Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr Met Val
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Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu Asn Gly
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Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr Ile Ser
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Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe Ile Ser
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Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln Ser Asn
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Asn Gly Arg Val Tyr Thr Ala Ser Asn Val Asn Thr Thr Asn Asn
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20 25 30		
acc ata caa gaa gaa tgg atg gag tgg aaa aaa gat aat cat agt tta		144
Thr Ile Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser Leu		
35 40 45		
tat gta gat cct att gtt gga act gtg gct agt ttt ctt tta aag aaa		192
Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys Lys		
50 55 60		
gtg ggg agt ctt gtt gga aaa aga ata ctg agt gag tta cgg aat tta		240
Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn Leu		
65 70 75 80		
ata ttt cct agt ggc agt aca aat cta atg caa gat att tta aga gag		288
Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg Glu		
85 90 95		
aca gaa aaa ttc ctg aat caa aga ctt aat aca gac act ctt gcc cgt		336
Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala Arg		
100 105 110		
gta aat gcg gaa ttg aca ggg ctg caa gca aat gta gaa gag ttt aat		384
Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe Asn		
115 120 125		
cga caa gta gat aat ttt ttg aac cct aac cga aat gct gtt cct tta		432
Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro Leu		
130 135 140		
tca ata act tct tca gtt aat aca atg cag caa tta ttt cta aat aga		480
Ser Ile Thr Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn Arg		
145 150 155 160		
tta acc cag ttc cag atg caa gga tac caa ttg tta tta tta cct tta		528
Leu Thr Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro Leu		
165 170 175		
ttt gca cag gca gcc aat tta cat ctt tct ttt att aga gat gtt att		576
Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val Ile		
180 185 190		
ctt aat gca gac gaa tgg gga att tca gca gca aca tta cgt acg tat		624
Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr Tyr		
195 200 205		
caa aat cac ctg aga aat tat aca aga gat tac tct aat tat tgt ata		672
Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys Ile		
210 215 220		

aat acg tat caa act gcg ttt aga ggt tta aac acc cgt tta cac gat		720
Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His Asp		
225	230	235
		240
atg tta gaa ttt aga aca tat atg ttt tta aat gta ttt gag tat gta		768
Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr Val		
245	250	255
tct atc tgg tcg ttg ttt aaa tat caa agc ctt cta gtc tct tct ggc		816
Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser Gly		
260	265	270
gct aat tta tat gca agt ggt agt gga cca cag cag acc caa tca ttt		864
Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser Phe		
275	280	285
act tca caa gac tgg cca ttt tta tat tct ctt ttc caa gtt aat tca		912
Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn Ser		
290	295	300
aat tat gtg tta aat ggc ttt agt ggc gct aga ctt acg cag act ttc		960
Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Thr Gln Thr Phe		
305	310	315
		320
cct aat att gtt ggt tta cct ggt act act aca act cac gca ttg ctt		1008
Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr His Ala Leu Leu		
325	330	335
gct gca agg gtc aat tac agt gga gga gtt tcg tct ggt gat ata ggc		1056
Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile Gly		
340	345	350
gct gtg ttt aat caa aat ttt agt tgt agc aca ttt ctc cca cct ttg		1104
Ala Val Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro Pro Leu		
355	360	365
tta aca cca ttt gtt agg agt tgg cta gat tca ggt tca gat cgg ggg		1152
Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp Arg Gly		
370	375	380
ggg atc aat acc gtt acc aat tgg caa aca gaa tcc ttt gag aca act		1200
Gly Ile Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu Thr Thr		
385	390	395
		400
tta ggt tta agg agt ggt gct ttt aca gct cga ggt aat tca aac tat		1248
Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser Asn Tyr		
405	410	415
tcc cca gat tat ttt atc cgt aat att tcc gga gtt cct tta gtt gtt		1296
Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu Val Val		
420	425	430
aga aat gaa gat tta aga aga ccg tta cac tat aat caa ata aga aat		1344
Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile Arg Asn		
435	440	445
ata gaa agt cct tca gga aca cct ggt gga tta cga gct tat atg gta		1392
Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr Met Val		
450	455	460
tct gtg cat aac aga aaa aat aat atc tat gcc gtt cat gaa aat ggt		1440

Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu Asn Gly			
465	470	475	480
act atg att cat tta gcg ccg gaa gat tat aca gga ttt act ata tcg			1488
Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr Ile Ser			
485	490	495	
ccg ata cat gca actcaa gtg aat aat caa acg cga aca ttt att tct			1536
Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe Ile Ser			
500	505	510	
gaa aaa ttt gga aat caa ggt gat tcc tta aga ttt gaa caa agc aac			1584
Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln Ser Asn			
515	520	525	
acg aca gct cgt tat aca ctt aga ggg aat gga aat agt tac aat ctt			1632
Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr Asn Leu			
530	535	540	
tat tta aga gta tct tca ata gga aat tcc act att cga gtt act ata			1680
Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val Thr Ile			
545	550	555	560
aac ggt aga gtt tat act gct tca aat gtt aat act act aca aat aac			1728
Asn Gly Arg Val Tyr Thr Ala Ser Asn Val Asn Thr Thr Asn Asn			
565	570	575	
gat gga gtt aat gat aat gga gct cgt ttt tca gat att aat att ggt			1776
Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn Ile Gly			
580	585	590	
aat gta gta gca agt gat aat act aat gta ccg tta gat ata aac gtg			1824
Asn Val Val Ala Ser Asp Asn Thr Asn Val Pro Leu Asp Ile Asn Val			
595	600	605	
aca tta aat tct ggt act caa ttt gag ctt atg aat att atg ttt gtt			1872
Thr Leu Asn Ser Gly Thr Gln Phe Glu Leu Met Asn Ile Met Phe Val			
610	615	620	
cca act aat atc tca cca ctt tat taa			1899
Pro Thr Asn Ile Ser Pro Leu Tyr			
625	630		

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 <212> PRT
 <213> *Bacillus thuringiensis*

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Met Asn Ser Val Leu Asn Ser Gly Arg Thr Thr Ile Cys Asp Ala Tyr			
1	5	10	15

Asn Val Val Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu Asp			
20	25	30	

Thr Ile Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser Leu			
35	40	45	

Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys Lys
50 55 60

Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn Leu
65 70 75 80

Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg Glu
85 90 95

Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala Arg
100 105 110

Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe Asn
115 120 125

Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro Leu
130 135 140

Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn Arg
145 150 155 160

Leu Thr Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro Leu
165 170 175

Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val Ile
180 185 190

Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr Tyr
195 200 205

Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys Ile
210 215 220

Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His Asp
225 230 235 240

Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr Val
245 250 255

Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser Gly
260 265 270

Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser Phe
275 280 285

Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn Ser
290 295 300

Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Thr Gln Thr Phe
305 310 315 320

Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr His Ala Leu Leu
325 330 335

Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile Gly
340 345 350

Ala Val Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro Pro Leu
355 360 365

Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp Arg Gly
370 375 380

Gly Ile Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu Thr Thr
385 390 395 400

Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser Asn Tyr
405 410 415

Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu Val Val
420 425 430

Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile Arg Asn
435 440 445

Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr Met Val
450 455 460

Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu Asn Gly
465 470 475 480

Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr Ile Ser
485 490 495

Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe Ile Ser
500 505 510

Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln Ser Asn
515 520 525

Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr Asn Leu
530 535 540

Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val Thr Ile
545 550 555 560

Asn Gly Arg Val Tyr Thr Ala Ser Asn Val Asn Thr Thr Asn Asn
565 570 575

Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn Ile Gly
580 585 590

Asn Val Val Ala Ser Asp Asn Thr Asn Val Pro Leu Asp Ile Asn Val
595 600 605

Thr Leu Asn Ser Gly Thr Gln Phe Glu Leu Met Asn Ile Met Phe Val
610 615 620

Pro Thr Asn Ile Ser Pro Leu Tyr
625 630

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<213> *Bacillus thuringiensis*

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Met Asn Asn Val Leu Asn Ser Glu Arg Thr Thr Lys Cys Gly Ala Tyr
1 5 10 15

aac gta gtg gct cat gat cca ttc agt ttt gaa cat aaa tca tta gat 96
Asn Val Val Ala His Asp Pro Phe Ser Phe Glu His Lys Ser Leu Asp
20 25 30

acc ata caa aaa gaa tgg atg gag tgg aaa aga act gat cat agt tta 144
Thr Ile Gln Lys Glu Trp Met Glu Trp Lys Arg Thr Asp His Ser Leu
35 40 45

tat gta tct cct att gta gga act ata gcc agt ttt ctg tta aag aaa 192
Tyr Val Ser Pro Ile Val Gly Thr Ile Ala Ser Phe Leu Leu Lys Lys
50 55 60

ata gga ggg ctt ata gga aaa aga ata tta agt gag tta aag aat tta 240
Ile Gly Gly Leu Ile Gly Lys Arg Ile Leu Ser Glu Leu Lys Asn Leu
65 70 75 80

att ttt cct agt ggt agt ata gaa tca atg caa gat att tta aga ggg 288

Ile Phe Pro Ser Gly Ser Ile Glu Ser Met Gln Asp Ile Leu Arg Gly			
85	90	95	
gca gaa caa ttt cta aat caa aga ctt gat gca gac acc ttt agt cgt			336
Ala Glu Gln Phe Leu Asn Gln Arg Leu Asp Ala Asp Thr Phe Ser Arg			
100	105	110	
gta gaa gca gaa ttg aga ggg ctt caa gca aat gta gag gaa ttt aat			384
Val Glu Ala Glu Leu Arg Gly Leu Gln Ala Asn Val Glu Glu Phe Asn			
115	120	125	
cga caa gtg gac aat ttt tta aac cca aat caa aac cct gcc cct tta			432
Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Gln Asn Pro Ala Pro Leu			
130	135	140	
gca ata att gat tcg gtt aat aca ttg caa caa tta ttc cta agt aga			480
Ala Ile Ile Asp Ser Val Asn Thr Leu Gln Gln Leu Phe Leu Ser Arg			
145	150	155	160
tta ccc cag ttc cag ata caa cgc tat cag cta tta tta tta cct tta			528
Leu Pro Gln Phe Gln Ile Gln Arg Tyr Gln Leu Leu Leu Pro Leu			
165	170	175	
ttt gca caa gca gcc aat tta cac ctt tct ttt att aga gac gtt att			576
Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val Ile			
180	185	190	
ctt aat gca gat gaa tgg gga ata cca gct gca acg gtg cgc aca tat			624
Leu Asn Ala Asp Glu Trp Gly Ile Pro Ala Ala Thr Val Arg Thr Tyr			
195	200	205	
aga gag cac cta caa aga tat aca cgc gaa tac tcc aat tat tgt ata			672
Arg Glu His Leu Gln Arg Tyr Thr Arg Glu Tyr Ser Asn Tyr Cys Ile			
210	215	220	
aat acg tat caa act gcg ttt aga ggg tta aat gcc act tta cac gat			720
Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Ala Thr Leu His Asp			
225	230	235	240
ttt cta gaa ttt aga aca tat atg ttt tta aat gta tta gac tat gta			768
Phe Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Leu Asp Tyr Val			
245	250	255	
tct atc tgg tcg ttg ttt aaa tat cag agc ctt ctg gta tcc tct ggc			816
Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser Gly			
260	265	270	
gct aat tta tat gcg agt ggt agt gga gta aca aat aga caa tca ttt			864
Ala Asn Leu Tyr Ala Ser Gly Ser Gly Val Thr Asn Arg Gln Ser Phe			
275	280	285	
act gca caa gac tgg cca ttt tta aat tct ctt ttc caa gtt aat caa			912
Thr Ala Gln Asp Trp Pro Phe Leu Asn Ser Leu Phe Gln Val Asn Gln			
290	295	300	
aat tat gta tta aca ggt atg aat ggt tat agg tat act tta agt tct			960
Asn Tyr Val Leu Thr Gly Met Asn Gly Tyr Arg Tyr Thr Leu Ser Ser			
305	310	315	320
gtt ttt ggt aca aat caa aca ata cat tct gtt agg agt aat tat agg			1008
Val Phe Gly Thr Asn Gln Thr Ile His Ser Val Arg Ser Asn Tyr Arg			

325	330	335	
ggc ggg gtt tca tct ggt tac att gga gtt aat ctt agt gaa ggt gac Gly Gly Val Ser Ser Gly Tyr Ile Gly Val Asn Leu Ser Glu Gly Asp 340	345	350	1056
caa aat ttt agt tgt agt aca ttt ttg gat cct tta gaa aca ccg ttt Gln Asn Phe Ser Cys Ser Thr Phe Leu Asp Pro Leu Glu Thr Pro Phe 355	360	365	1104
att aga agt tgg ctg gat tca ggt agc gat gat ggc ttt aat tgg agt Ile Arg Ser Trp Leu Asp Ser Gly Ser Asp Asp Gly Phe Asn Trp Ser 370	375	380	1152
aca gga gtc ttt aca aca act att ggt tta cct act tgt agc att ttt Thr Gly Val Phe Thr Thr Ile Gly Leu Pro Thr Cys Ser Ile Phe 385	390	395	1200
tgg cct cgt ggt aac tcg aac tat ttt cca gat tat ttt ata cga aat Trp Pro Arg Gly Asn Ser Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn 405	410	415	1248
att tct ggt gtc gtt ggt cgt ctt agg aac gaa gat tta aga aga cca Ile Ser Gly Val Val Gly Arg Leu Arg Asn Glu Asp Leu Arg Arg Pro 420	425	430	1296
cta tat ttt aat gag ata aga aat ata gta gga aat aac aat cca ccg Leu Tyr Phe Asn Glu Ile Arg Asn Ile Val Gly Asn Asn Pro Pro 435	440	445	1344
gca act gga tcg tta tca gtc gcc agc cta gtc tct gtg cat aac aga Ala Thr Gly Ser Leu Ser Val Ala Ser Leu Val Ser Val His Asn Arg 450	455	460	1392
aaa aat aat att tat gct gct cat gaa aat ggt act atg att cat ttg Lys Asn Asn Ile Tyr Ala Ala His Glu Asn Gly Thr Met Ile His Leu 465	470	475	1440
gca ccg gaa gat tat aca ggt ttc aca atg tca cca ata cat gca act Ala Pro Glu Asp Tyr Thr Gly Phe Thr Met Ser Pro Ile His Ala Thr 485	490	495	1488
caa gta aat aat caa aca cga aca ttt att tcc gag aaa tta gga aac Gln Val Asn Asn Gln Thr Arg Thr Phe Ile Ser Glu Lys Leu Gly Asn 500	505	510	1536
caa ggt gat tcc ttg aga ttt gaa caa aca aat aca acg gct cga tac Gln Gly Asp Ser Leu Arg Phe Glu Gln Thr Asn Thr Ala Arg Tyr 515	520	525	1584
aca ttt aga ggg aat gga aat agt tac aat ctt tat tta aga gta tct Thr Phe Arg Gly Asn Ser Tyr Asn Leu Tyr Leu Arg Val Ser 530	535	540	1632
tca cta gga aat tcc aca att cga gtt act ata aac ggt aga gtt tat Ser Leu Gly Asn Ser Thr Ile Arg Val Thr Ile Asn Gly Arg Val Tyr 545	550	555	1680
act gtt tca aac gtc aat act act aca aat aac gat gga gtt gtt gat Thr Val Ser Asn Val Asn Thr Thr Asn Asn Asp Gly Val Val Asp 565	570	575	1728

aat ggc gct cgt ttt tca gat att aat ata ggt aat gta gtg gca agt Asn Gly Ala Arg Phe Ser Asp Ile Asn Ile Gly Asn Val Val Ala Ser 580 585 590	1776
gct aat act aat ata cca tta gat ata aat gta aca ttt aac tct ggt Ala Asn Thr Asn Ile Pro Leu Asp Ile Asn Val Thr Phe Asn Ser Gly 595 600 605	1824
acg caa ttt gag ctt atg aat att atg ttt gtt cca act aat att cca Thr Gln Phe Glu Leu Met Asn Ile Met Phe Val Pro Thr Asn Ile Pro 610 615 620	1872
cca att tat taa Pro Ile Tyr 625	1884
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Asn Val Val Ala His Asp Pro Phe Ser Phe Glu His Lys Ser Leu Asp 20 25 30	
Thr Ile Gln Lys Glu Trp Met Glu Trp Lys Arg Thr Asp His Ser Leu 35 40 45	
Tyr Val Ser Pro Ile Val Gly Thr Ile Ala Ser Phe Leu Leu Lys Lys 50 55 60	
Ile Gly Gly Leu Ile Gly Lys Arg Ile Leu Ser Glu Leu Lys Asn Leu 65 70 75 80	
Ile Phe Pro Ser Gly Ser Ile Glu Ser Met Gln Asp Ile Leu Arg Gly 85 90 95	
Ala Glu Gln Phe Leu Asn Gln Arg Leu Asp Ala Asp Thr Phe Ser Arg 100 105 110	
Val Glu Ala Glu Leu Arg Gly Leu Gln Ala Asn Val Glu Glu Phe Asn 115 120 125	
Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Gln Asn Pro Ala Pro Leu 130 135 140	

Ala Ile Ile Asp Ser Val Asn Thr Leu Gln Gln Leu Phe Leu Ser Arg
145 150 155 160

Leu Pro Gln Phe Gln Ile Gln Arg Tyr Gln Leu Leu Leu Leu Pro Leu
165 170 175

Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val Ile
180 185 190

Leu Asn Ala Asp Glu Trp Gly Ile Pro Ala Ala Thr Val Arg Thr Tyr
195 200 205

Arg Glu His Leu Gln Arg Tyr Thr Arg Glu Tyr Ser Asn Tyr Cys Ile
210 215 220

Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Ala Thr Leu His Asp
225 230 235 240

Phe Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Leu Asp Tyr Val
245 250 255

Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser Gly
260 265 270

Ala Asn Leu Tyr Ala Ser Gly Ser Gly Val Thr Asn Arg Gln Ser Phe
275 280 285

Thr Ala Gln Asp Trp Pro Phe Leu Asn Ser Leu Phe Gln Val Asn Gln
290 295 300

Asn Tyr Val Leu Thr Gly Met Asn Gly Tyr Arg Tyr Thr Leu Ser Ser
305 310 315 320

Val Phe Gly Thr Asn Gln Thr Ile His Ser Val Arg Ser Asn Tyr Arg
325 330 335

Gly Gly Val Ser Ser Gly Tyr Ile Gly Val Asn Leu Ser Glu Gly Asp
340 345 350

Gln Asn Phe Ser Cys Ser Thr Phe Leu Asp Pro Leu Glu Thr Pro Phe
355 360 365

Ile Arg Ser Trp Leu Asp Ser Gly Ser Asp Asp Gly Phe Asn Trp Ser
370 375 380

Thr Gly Val Phe Thr Thr Ile Gly Leu Pro Thr Cys Ser Ile Phe

385

390

395

400

Trp Pro Arg Gly Asn Ser Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn
405 410 415

Ile Ser Gly Val Val Gly Arg Leu Arg Asn Glu Asp Leu Arg Arg Pro
420 425 430

Leu Tyr Phe Asn Glu Ile Arg Asn Ile Val Gly Asn Asn Asn Pro Pro
435 440 445

Ala Thr Gly Ser Leu Ser Val Ala Ser Leu Val Ser Val His Asn Arg
450 455 460

Lys Asn Asn Ile Tyr Ala Ala His Glu Asn Gly Thr Met Ile His Leu
465 470 475 480

Ala Pro Glu Asp Tyr Thr Gly Phe Thr Met Ser Pro Ile His Ala Thr
485 490 495

Gln Val Asn Asn Gln Thr Arg Thr Phe Ile Ser Glu Lys Leu Gly Asn
500 505 510

Gln Gly Asp Ser Leu Arg Phe Glu Gln Thr Asn Thr Thr Ala Arg Tyr
515 520 525

Thr Phe Arg Gly Asn Gly Asn Ser Tyr Asn Leu Tyr Leu Arg Val Ser
530 535 540

Ser Leu Gly Asn Ser Thr Ile Arg Val Thr Ile Asn Gly Arg Val Tyr
545 550 555 560

Thr Val Ser Asn Val Asn Thr Thr Asn Asn Asp Gly Val Val Asp
565 570 575

Asn Gly Ala Arg Phe Ser Asp Ile Asn Ile Gly Asn Val Val Ala Ser
580 585 590

Ala Asn Thr Asn Ile Pro Leu Asp Ile Asn Val Thr Phe Asn Ser Gly
595 600 605

Thr Gln Phe Glu Leu Met Asn Ile Met Phe Val Pro Thr Asn Ile Pro
610 615 620

Pro Ile Tyr
625

<210> 7
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<212> DNA
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<220>
<223> artificial cry2Ae DNA sequence for expression in cotton

<220>
<221> CDS
<222> (3)..(1901)
<223>

<400> 7

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1 5 10 15

gca tac aac gtt gtt gct cat gat cct ttc tct ttc gag cat aag tct 95
Ala Tyr Asn Val Val Ala His Asp Pro Phe Ser Phe Glu His Lys Ser
20 25 30

ctt gat aca att agg aag gag tgg atg gag tgg aag agg act gat cat 143
Leu Asp Thr Ile Arg Lys Glu Trp Met Glu Trp Lys Arg Thr Asp His
35 40 45

tct ctt tac gtt gct cct att gtt ggt act gtt tct tct ttc ctt ctt 191
Ser Leu Tyr Val Ala Pro Ile Val Gly Thr Val Ser Ser Phe Leu Leu
50 55 60

aag aag gtt tct ctt atc ggt aag agg atc ctt tct gag ctt tgg 239
Lys Lys Val Gly Ser Leu Ile Gly Lys Arg Ile Leu Ser Glu Leu Trp
65 70 75

ggt ctt atc ttc cct tct ggt tct act aac ctt atg caa gat att ctt 287
Gly Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu
80 85 90 95

agg gag act gaa caa ttc ctt aac cag agg ctt aac act gat act ctt 335
Arg Glu Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu
100 105 110

gct agg gtt aac gct gag ctt gag ggt ctt caa gct aac att agg gaa 383
Ala Arg Val Asn Ala Glu Leu Glu Gly Leu Gln Ala Asn Ile Arg Glu
115 120 125

ttc aac cag caa gtt gat aac ttc ctt aac cct act caa aac cct gtt 431
Phe Asn Gln Gln Val Asp Asn Phe Leu Asn Pro Thr Gln Asn Pro Val
130 135 140

cct ctt tct att act tct tct gtt aac act atg caa caa ctt ttc ctt 479
Pro Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu
145 150 155

aac agg ctt cct caa ttc agg gtt caa ggt tac caa ctt ctt ctt 527
Asn Arg Leu Pro Gln Phe Arg Val Gln Gly Tyr Gln Leu Leu Leu
160 165 170 175

cct ctt ttc gct caa gct gct aac atg cac cta agc ttc att agg gat Pro Leu Phe Ala Gln Ala Ala Asn Met His Leu Ser Phe Ile Arg Asp 180 185 190	575
gtt gtt ctt aac gct gat gag tgg ggt att tct gct gct act ctt agg Val Val Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg 195 200 205	623
act tac caa aac tac ctt aag aac tac act act gag tac tct aac tac Thr Tyr Gln Asn Tyr Leu Lys Asn Tyr Thr Glu Tyr Ser Asn Tyr 210 215 220	671
tgc att aac act tac caa act gct ttc agg ggt ctt aac act agg ctt Cys Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu 225 230 235	719
cat gat atg ctt gag ttc agg act tac atg ttc ctt aac gtt ttc gag His Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu 240 245 250 255	767
tac gtt tct att tgg tct ctt ttc aag tac cag tct ctt gtt tct Tyr Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser 260 265 270	815
tct ggt gct aac ctt tac gct tct ggt tct ggt cct caa caa act caa Ser Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln 275 280 285	863
tct ttc act tct caa gac tgg cct ttc ctt tac tct ctt ttc caa gtt Ser Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val 290 295 300	911
aac tct aac tac gtt ctt aac ggt ttc tct ggt gct agg ctt act caa Asn Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Thr Gln 305 310 315	959
act ttc cct aac atc ggt ggt ctt cct ggt act act act act cat gct Thr Phe Pro Asn Ile Gly Gly Leu Pro Gly Thr Thr Thr His Ala 320 325 330 335	1007
ctt ctt gct gct agg gtt aac tac tct ggt ggt gtt tct tct ggt gat Leu Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp 340 345 350	1055
atc ggt gct gtt ttc aac cag aac ttc tct tgc tct act ttc ctt cct Ile Gly Ala Val Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro 355 360 365	1103
cct ctt ctt act cct ttc gtt agg tct tgg ctt gat tct ggt tct gat Pro Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp 370 375 380	1151
agg ggt ggt gtt aac act gtt act aac tgg caa act gag tct ttc gag Arg Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu 385 390 395	1199
tct act ctt ggt ctt agg tgc ggt gct ttc act gct agg ggt aac tct Ser Thr Leu Gly Leu Arg Cys Gly Ala Phe Thr Ala Arg Gly Asn Ser 400 405 410 415	1247
aac tac ttc cct gat tac ttc att agg aac att tct ggt gtt cct ctt	1295

Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu			
420	425	430	
gtt gtt agg aac gag gat ctt agg agg cct ctt cat tac aac gag att			1343
Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile			
435	440	445	
agg aac att gag tct cct tct ggt act cct ggt ggt ctt agg gct tac			1391
Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr			
450	455	460	
atg gtt tct gtt cat aac agg aag aac atc tac gct gtt cat gag			1439
Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu			
465	470	475	
aac ggt act atg att cat ctt gct cct gag gat tac acc ggt ttc acc			1487
Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr			
480	485	490	495
atc tcc ccc atc cac gcc acc cag gtc aat aat cag acc agg acc ttc			1535
Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe			
500	505	510	
atc tcc gag aag ttc ggc aac cag ggc gac tcc ctg agg ttc gag cag			1583
Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln			
515	520	525	
tcc aac acc acc gcc agg tac acc ctg agg ggc aac ggc aac tcc tac			1631
Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr			
530	535	540	
aac ctg tac ctc agg gtg tcc tcc ctc ggc aac tcc acc atc agg gtc			1679
Asn Leu Tyr Leu Arg Val Ser Ser Leu Gly Asn Ser Thr Ile Arg Val			
545	550	555	
acc atc aac ggc agg gtg tac acc gcc tcc aac gtg aac acc acc acc			1727
Thr Ile Asn Gly Arg Val Tyr Thr Ala Ser Asn Val Asn Thr Thr Thr			
560	565	570	575
aac aac gac ggc gtc aac gac aac ggc gct agg ttc ctg gac atc aac			1775
Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Leu Asp Ile Asn			
580	585	590	
atg ggc aac gtc gtg gcc tcc gac aac acc aac gtg ccc ctg gac atc			1823
Met Gly Asn Val Ala Ser Asp Asn Thr Asn Val Pro Leu Asp Ile			
595	600	605	
aac gtg aca ttt aac tcc ggc acc cag ttc gag ctg atg aac atc atg			1871
Asn Val Thr Phe Asn Ser Gly Thr Gln Phe Glu Leu Met Asn Ile Met			
610	615	620	
ttc gtg cca act aac ctc cca ccc atc tac tgagctagc			1910
Phe Val Pro Thr Asn Leu Pro Pro Ile Tyr			
625	630		

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 <212> PRT
 <213> Unknown

<220>

<223> Artificial Sequence

<400> 8

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Tyr Asn Val Val Ala His Asp Pro Phe Ser Phe Glu His Lys Ser Leu
20 25 30

Asp Thr Ile Arg Lys Glu Trp Met Glu Trp Lys Arg Thr Asp His Ser
35 40 45

Leu Tyr Val Ala Pro Ile Val Gly Thr Val Ser Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Ile Gly Lys Arg Ile Leu Ser Glu Leu Trp Gly
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Glu Gly Leu Gln Ala Asn Ile Arg Glu Phe
115 120 125

Asn Gln Gln Val Asp Asn Phe Leu Asn Pro Thr Gln Asn Pro Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Arg Val Gln Gly Tyr Gln Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Met His Leu Ser Phe Ile Arg Asp Val
180 185 190

Val Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asn Tyr Leu Lys Asn Tyr Thr Thr Glu Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Thr Gln Thr
305 310 315 320

Phe Pro Asn Ile Gly Gly Leu Pro Gly Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Val Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro Pro
355 360 365

Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp Arg
370 375 380

Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu Ser
385 390 395 400

Thr Leu Gly Leu Arg Cys Gly Ala Phe Thr Ala Arg Gly Asn Ser Asn
405 410 415

Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu Val
420 425 430

Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile Arg
435 440 445

Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr Met
450 455 460

Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu Asn

465

470

475

480

Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr Ile
485 490 495

Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe Ile
500 505 510

Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln Ser
515 520 525

Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Ser Tyr Asn
530 535 540

Leu Tyr Leu Arg Val Ser Ser Leu Gly Asn Ser Thr Ile Arg Val Thr
545 550 555 560

Ile Asn Gly Arg Val Tyr Thr Ala Ser Asn Val Asn Thr Thr Thr Asn
565 570 575

Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Leu Asp Ile Asn Met
580 585 590

Gly Asn Val Val Ala Ser Asp Asn Thr Asn Val Pro Leu Asp Ile Asn
595 600 605

Val Thr Phe Asn Ser Gly Thr Gln Phe Glu Leu Met Asn Ile Met Phe
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Val Pro Thr Asn Leu Pro Pro Ile Tyr
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<211> 1910

<212> DNA

<213> Unknown

<220>

<223> artificial cry2Ae DNA sequence for expression in corn

<400> 9

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tggagtgaaa gcgcacccgac cacagcctgt acgtggcccc tatcgtgggc accgtgagca	180
gcttcctgct gaagaaggta ggcagcctga tcggcaagag gatcctgagc gagctgtggg	240
gcctgatctt cccaaaggcgc agcaccaacc tggatgcagga catcctgagg gagaccgagc	300

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